



SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> P04885US1

<140> 09/833,017

<141> 2001-04-10

<150> PCT/CA00/00605

<151> 2000-05-25

<150> 2,302,861

<151> 2000-04-10

<150> 2,332,733

<151> 2001-02-20

<160> 28

<170> PatentIn version 3.0

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1 5 10 15  
  
gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96  
Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30  
  
ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141  
Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<211> 46

<212> PRT

<213> Streptococcus mutans

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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1 5 10 15

acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96  
Thr Val Leu Phe Leu Leu Phe Leu Ser Lys Val Ser Asn Val Thr  
20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144  
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile  
35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192  
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu  
50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser			
65	70	75	80
ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac			288
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp			
85	90	95	
ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga			336
Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly			
100	105	110	
att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca			384
Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala			
115	120	125	
gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att			432
Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile			
130	135	140	
ggc cgt ctt aaa gat agt ttg acc aag atg aag gtc aaa aaa cgc ttg			480
Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu			
145	150	155	160
att cca atg aat att act atg ctt cta tac tac ctt tta ata cag gta			528
Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val			
165	170	175	
ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt			576
Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg			
180	185	190	
aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca			624
Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser			
195	200	205	
ttt tta agc caa tat acc aaa caa aag gtt caa aat gag ata atg gca			672
Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala			
210	215	220	
caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata			720
Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile			
225	230	235	240
gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat			768
Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn			
245	250	255	
att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt			816
Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser			
260	265	270	
att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg			864
Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu			
275	280	285	
cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat			912
Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp			

290	295	300	
gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa			
Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys			960
305	310	315	320
aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag			
Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu			1008
325	330	335	
atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat			
Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn			1056
340	345	350	
gcc att gag gct gtc ttc gaa tca tta aat cct gaa att cag tta gcc			
Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala			1104
355	360	365	
ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc			
Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr			1152
370	375	380	
aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc			
Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser			1200
385	390	395	400
act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att			
Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile			1248
405	410	415	
ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat			
Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His			1296
420	425	430	
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Leu Phe Lys Gln Leu Leu Ile Ile Lys			1326
435	440		
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Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr			
20	25	30	

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile  
35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu  
50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser  
65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp  
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly  
100 105 110

Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala  
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile  
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu  
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val  
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg  
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser  
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala  
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile  
225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn  
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser  
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu  
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp  
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys  
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu  
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn  
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala  
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr  
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser  
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile  
405 410 415

Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His  
420 425 430

Leu Phe Lys Gln Leu Leu Ile Ile Lys  
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195	200	205	
gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg			672
210	215	220	
aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg			720
225	230	235	240
gct gtg att gct gat caa agg aga gca aaa Ala Val Ile Ala Asp Gln Arg Arg Ala Lys			750
245	250		
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Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr 20 25 30			
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile 35 40 45			
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys 50 55 60			
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His 65 70 75 80			
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met 85 90 95			
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys 100 105 110			

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr  
115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe  
130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile  
145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr  
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys  
180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro  
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg  
210 215 220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg  
225 230 235 240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys  
245 250

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<213> Streptococcus mutans

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<222> (1)..(46)

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<222> (1)..(46)

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1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<222> (1)..(46)

<400> 9

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1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
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1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe  
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala  
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1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<213> Streptococcus mutans

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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
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<222> (1)..(46)

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20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<213> synthetic construct

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<222> (1)..(21)

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Gln Ala Leu Gly Lys  
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<213> synthetic construct

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<222> (1)..(19)

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<210> 17

<211> 24

<212> DNA

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<222> (1)..(24)

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21

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21

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<212> DNA

<213> *Streptococcus mutans*

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<221> CDS

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1 5 10 15		
tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat	96	
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp		
20 25 30		
tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat	144	
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His		
35 40 45		
cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca	192	
Pro Glu Leu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr		
50 55 60		
cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag	240	
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln		
65 70 75 80		
aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa	288	
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu		
85 90 95		
cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt	336	
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe		
100 105 110		
cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa	384	
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln		
115 120 125		
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<212> PRT

<213> Streptococcus mutans

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Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His  
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr  
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln  
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu  
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe  
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln  
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala  
130 135

<210> 24

<211> 680

<212> DNA

<213> Streptococcus mutans

<220>

<221> misc\_feature

<222> (1)..(680)

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tttataataa ttttattata aaaggaggc atcgtaatag atggaagaag attttcaa 120  
tgttttaat aaggtaaagc caattgtatg gaaatthaagc cgtttattact ttatcaa 180  
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240  
acatccagaa ttagaagagg atgatacataa attgtatatac tatttaaga cacgttttc 300  
taattacatt aaagatgtt tgcgtcagca agaaagttagtca aacgtcgtt ttaatagaat 360  
gtcttatgaa gaagtccgtg agattgaaca ctgttgtca agtggcggtt tgcaattgg 420  
tgaatataatt ttatcggt atagtttgct tgcataataa caaggctgtt gtactgaaaa 480  
gcaagagctg tttgagcgct tggtagcagg agagcactt ttggaaaggc aaagtatgct 540  
gaaagattta cgtaaaaat taagtgatt taaggaaaa tagttaaaaa gggaaagaat 600  
ggaacatgtt attgtaccat tcttttggt tgaaaattaa gaaaagtttataaattat 660  
tggtttaaca tgccatatta 680

<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(2280)

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Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile  
1 5 10 15  
ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96  
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser  
20 25 30  
tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144  
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg

35	40	45	
cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala	50	55	60
gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala	65	70	75
----- tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu	85	90	95
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile	100	105	110
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe	115	120	125
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val	130	135	140
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser	145	150	155
160			
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr	165	170	175
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys	180	185	190
195			
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln	200	205	
220			
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc Lys Ala Leu Met Thr Tyr Ile Ile Ala Ser Leu Ile Val Thr Leu	210	215	
220			
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr	225	230	
235			
240			
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu	245	250	
255			
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr	260	265	
270			
816			

ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser 275 280 285	864
tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg 290 295 300	912
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cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile 305 310 315 320	960
gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met 325 330 335	1008
gta att ttg gtt ggt ggg gtt ttg ttg gcg caa aac aat aac ctt ttc Val Ile Leu Val Gly Gly Val Leu Ala Gln Asn Asn Asn Leu Phe 340 345 350	1056
ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala 355 360 365	1104
ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn 370 375 380	1152
gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc Ala Val Val Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr 385 390 395 400	1200
att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser 405 410 415	1248
gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser 420 425 430	1296
gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val 435 440 445	1344
gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser 450 455 460	1392
gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn 465 470 475 480	1440
cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg 485 490 495	1488

gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe 500 505 510	1536
gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile 515 520 525	1584
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu 530 535 540	1632
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545 550 555 560	1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565 570 575	1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580 585 590	1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595 600 605	1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610 615 620	1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625 630 635 640	1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645 650 655	1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660 665 670	2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675 680 685	2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690 695 700	2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705 710 715 720	2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat gag	2208

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln  
725 730 735

gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa 2256  
Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln  
740 745 750

ggt ttc tat tat aac ctg ttt aat 2280  
Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile  
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Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser  
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg  
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala  
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala  
65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu  
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile  
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe  
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val

130

135

140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser  
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr  
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys  
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln  
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu  
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr  
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu  
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr  
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser  
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg  
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile  
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met  
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe  
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala  
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn  
370 375 380

Ala Val Val Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr  
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser  
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser  
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val  
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser  
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn  
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg  
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe  
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile  
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu  
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val  
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn  
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu  
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro  
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu  
610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu  
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln  
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg  
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu  
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile  
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His  
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln  
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln  
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

<210> 27

<211> 900

<212> DNA

<213> *Streptococcus mutans*

<220>

<221> CDS

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 Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr  
 1 5 10 15  
  
 cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc 96  
 His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile  
 20 25 30  
  
 ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att 144  
 Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile  
 35 40 45  
  
 tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct 192  
 Ser Thr Gly Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser  
 50 55 60  
  
 tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct 240  
 Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala  
 65 70 75 80  
  
 gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca 288  
 Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro  
 85 90 95  
  
 aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga 336  
 Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg  
 100 105 110  
  
 gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag 384  
 Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys  
 115 120 125  
  
 tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac 432  
 Ser Lys Ser Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp  
 130 135 140  
  
 aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att 480  
 Lys Glu Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile  
 145 150 155 160  
  
 ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt 528  
 Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly  
 165 170 175  
  
 gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat 576  
 Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp  
 180 185 190  
  
 att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat 624  
 Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp

195	200	205	
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu			672
210	215	220	
aaa aag gga aat gac aag gtt att gaa gga aaa att aac aat gtc Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val			720
225	230	235	240
gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr			768
245	250	255	
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly			816
260	265	270	
atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp			864
275	280	285	
tat ttc aaa gat aaa tta ctg cat aaa atg gat aat Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn			900
290	295	300	
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Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr			
1	5	10	15
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile			
20	25	30	
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile			
35	40	45	
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser			
50	55	60	
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala			
65	70	75	80

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro  
85 90 95

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg  
100 105 110

Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys  
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp  
130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile  
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly  
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp  
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp  
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu  
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val  
225 230 235 240

Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr  
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly  
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp  
275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn  
290 295 300